

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/552,287  
Source: pu/10  
Date Processed by STIC: 10/18/05

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/552,287

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
     Wrapped Aminos        was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will  
                               prevent "wrapping."
  
- 2      Invalid Line Length    The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino        The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers;  
     Numbering                use **space characters**, instead.
  
- 4      Non-ASCII                The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please  
                               ensure your subsequent submission is saved in **ASCII** text.
  
- 5      Variable Length        Sequence(s)          contain n's or Xaa's representing more than one residue. **Per Sequence Rules**,  
                               each n or Xaa can only represent a single residue. Please present the **maximum** number of each  
                               residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0            A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
     "bug"                      sequences(s)         . Normally, PatentIn would automatically generate this section from the  
                               previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to  
                               the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for**  
                               **Artificial or Unknown sequences.**
  
- 7      Skipped Sequences      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
     (OLD RULES)                (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                     (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                     (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                     This sequence is intentionally skipped  
  
                               Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8      Skipped Sequences      Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence.  
     (NEW RULES)                <210> sequence id number  
                                     <400> sequence id number  
                                     000
  
- 9      Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     (NEW RULES)                Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                                     In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10      Invalid <213>          Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or  
     Response                    scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or  
                                     is Artificial Sequence
  
- 11      Use of <220>            Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
                                     Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or  
                                     "Unknown." Please explain source of genetic material in <220> to <223> section.  
                                     (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0            Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
     "bug"                      resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
                                     listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13      Misuse of n/Xaa        "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



PCT

## RAW SEQUENCE LISTING

DATE: 10/18/2005

PATENT APPLICATION: US/10/552,287

TIME: 10:13:33

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\10182005\J552287.raw

3 <110> APPLICANT: Futerman, Anthony  
 4 Sussman, Joel  
 5 Silman, Israel  
 6 Harel, Michal  
 7 Dvir, Hay  
 8 Toker, Lilly  
 9 Swetlana Adamsky  
 11 <120> TITLE OF INVENTION: GAUCHER DISEASE DRUGS AND METHODS OF IDENTIFYING SAME  
 13 <130> FILE REFERENCE: 30227  
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/552,287  
 C--> 15 <141> CURRENT FILING DATE: 2005-10-04  
 15 <160> NUMBER OF SEQ ID NOS: 16  
 17 <170> SOFTWARE: PatentIn version 3.2

*See item 4 on Euro summary sheet*

## ERRORED SEQUENCES

2007 <210> SEQ ID NO: 16  
 2008 <211> LENGTH: 497  
 2009 <212> TYPE: PRT  
 2010 <213> ORGANISM: Pan troglodytes  
 2012 <400> SEQUENCE: 16  
 2014 Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys  
 2015 1 5 10 15  
 2018 Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro  
 2019 20 25 30  
 2022 Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg  
 2023 35 40 45  
 2026 Met Glu Leu Ser Met Gly Thr Ile Gln Ala Asn His Thr Gly Thr Gly  
 2027 50 55 60  
 2030 Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly  
 2031 65 70 75 80  
 2034 Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu  
 2035 85 90 95  
 2038 Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu Glu  
 2039 100 105 110  
 2042 Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe  
 2043 115 120 125  
 2046 Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu  
 2047 130 135 140  
 2050 His Asn Phe Ser Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu  
 2051 145 150 155 160  
 2054 Ile His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser Leu Leu Ala

*P.2*

**Does Not Comply  
 Corrected Diskette Needed**

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/552,287

DATE: 10/18/2005

TIME: 10:13:33

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\10182005\J552287.raw

2055				165					170					175		
2058	Ser	Pro	Trp	Thr	Ser	Pro	Thr	Trp	Leu	Lys	Thr	Asn	Gly	Ala	Val	Asn
2059				180					185					190		
2062	Gly	Lys	Gly	Ser	Leu	Lys	Gly	Gln	Pro	Gly	Asp	Ile	Tyr	His	Gln	Thr
2063				195				200					205			
2066	Trp	Ala	Arg	Tyr	Phe	Val	Lys	Phe	Leu	Asp	Ala	Tyr	Ala	Glu	His	Lys
2067		210					215				220					
2070	Leu	Gln	Phe	Trp	Ala	Val	Thr	Ala	Glu	Asn	Glu	Pro	Ser	Ala	Gly	Leu
2071	225					230				235					240	
2074	Leu	Ser	Gly	Tyr	Pro	Phe	Gln	Cys	Leu	Gly	Phe	Thr	Pro	Glu	His	Gln
2075				245					250					255		
2078	Arg	Asp	Phe	Ile	Ala	Arg	Asp	Leu	Gly	Pro	Thr	Leu	Ala	Asn	Ser	Thr
2079			260					265				270				
2082	His	His	Asn	Val	Arg	Leu	Leu	Met	Leu	Asp	Asp	Gln	Arg	Leu	Leu	Leu
2083			275				280					285				
2086	Pro	His	Trp	Ala	Lys	Val	Val	Leu	Thr	Asp	Pro	Glu	Ala	Ala	Lys	Tyr
2087		290					295				300					
2090	Val	His	Gly	Ile	Ala	Val	His	Trp	Tyr	Leu	Asp	Phe	Leu	Ala	Pro	Ala
2091	305					310				315					320	
2094	Lys	Ala	Thr	Leu	Gly	Glu	Thr	His	Arg	Leu	Phe	Pro	Asn	Thr	Met	Leu
2095				325					330					335		
2098	Phe	Ala	Ser	Glu	Ala	Cys	Val	Gly	Ser	Lys	Phe	Trp	Glu	Gln	Ser	Val
2099			340					345				350				
2102	Arg	Leu	Gly	Ser	Trp	Asp	Arg	Gly	Met	Gln	Tyr	Ser	His	Ser	Ile	Ile
2103			355				360				365					
2106	Thr	Asn	Leu	Leu	Tyr	His	Val	Val	Gly	Trp	Thr	Asp	Trp	Asn	Leu	Ala
2107		370					375				380					
2110	Leu	Asn	Pro	Glu	Gly	Gly	Pro	Asn	Trp	Val	Arg	Asn	Phe	Val	Asp	Ser
2111	385					390				395					400	
2114	Pro	Ile	Ile	Val	Asp	Ile	Thr	Lys	Asp	Thr	Phe	Tyr	Lys	Gln	Pro	Met
2115			405						410					415		
2118	Phe	Tyr	His	Leu	Gly	His	Phe	Ser	Lys	Phe	Ile	Pro	Glu	Gly	Ser	Gln
2119			420					425				430				
2122	Arg	Val	Gly	Leu	Val	Ala	Ser	Gln	Lys	Asn	Asp	Leu	Asp	Ala	Val	Ala
2123			435					440				445				
2126	Leu	Met	His	Pro	Asp	Gly	Ser	Ala	Val	Val	Val	Val	Leu	Asn	Arg	Ser
2127		450				455				460						
2130	Ser	Lys	Asp	Val	Pro	Leu	Thr	Ile	Lys	Asp	Pro	Ala	Val	Gly	Phe	Leu
2131	465					470				475					480	
2134	Glu	Thr	Ile	Ser	Pro	Gly	Tyr	Ser	Ile	His	Thr	Tyr	Leu	Trp	Arg	Arg
2135				485				490				495				
2138	Gln															

E--&gt; 2147

①

*delete**see pg 3, 5-6*

10/552,287 3

<210> 7  
<211> 497  
<212> PRT  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (496)..(496)  
<223> Arg to His mutant  
    - = =  
<400> 7

(why is Arg listed in location 496 instead of His?)  
see p.5

Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys  
1                    5                    10                    15

Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro  
                    20                    25                    30

Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg  
                    35                    40                    45

Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly  
                    50                    55                    60

Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly  
65                    70                    75                    80

Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu  
                    85                    90                    95

Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu Glu  
                    100                    105                    110

Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe  
                    115                    120                    125

Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu  
                    130                    135                    140

His Asn Phe Ser Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu  
145                    150                    155                    160

Ile His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser Leu Leu Ala  
                    165                    170                    175

10/552,287 4

Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys Thr Asn Gly Ala Val Asn  
180 185 190

Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr His Gln Thr  
195 200 205

Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu His Lys  
210 215 220

Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu  
225 230 235 240

Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln  
245 250 255

Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr  
260 265 270

His His Asn Val Arg Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu  
275 280 285

Pro His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr  
290 295 300

Val His Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala  
305 310 315 320

Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu  
325 330 335

Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val  
340 345 350

Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile  
355 360 365

Thr Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala  
370 375 380

Leu Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser  
385 390 395 400

Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met

10/552,287

5

405

410

415

Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln  
420 425 430

Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala  
435 440 445

Leu Met Asn Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg Ser  
450 455 460

Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu  
465 470 475 480

Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg  
485 490 495

same error  
in sequence 14

10/552,287

6

<210> 9  
<211> 497  
<212> PRT  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (370)..(370)  
<223> Asn Q Ser mutant

to



**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/552,287

DATE: 10/18/2005

TIME: 10:13:34

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\10182005\J552287.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:2002 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0

L:2147 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16